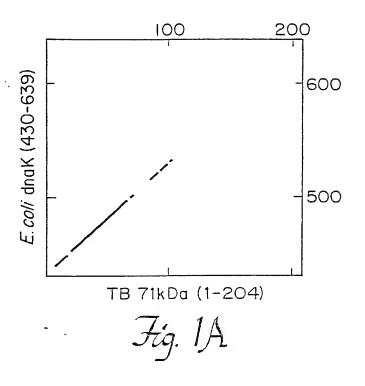
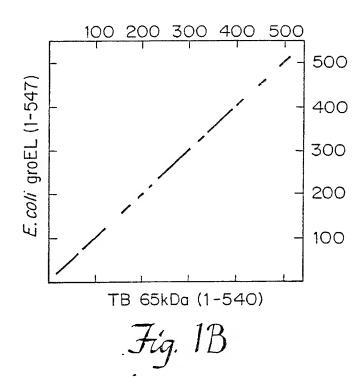


App No.: 10/046,649

Title: Stress Proteins and Uses Therefor

Inventors: Richard A. Young, et al.







	·	70	20	30	40	50	09	7.0
HUMP1	MLRLP	TVFRQMRPV	SRVLAPHLTR	AYAKDVKFGA	DARALMLQG	SVDLLADAVAV	TVFRQMRPVSRVLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTVIIEQSWGS	IEQSWGS
GROEL			MA	AKDVKFGN	IDARVKMLRG	VNVLADAVKV	AKDVKFGNDARVKMLRGVNVLADAVKVTLGPKGRNVVLDKSFGA	LDKSFGA
	71	80	06	100	110	120	130	140
HUMP1 GROEL	PKVTK : :: PTITK	DGVTVAKSI:::::DGVSVAREI	DLKDKYKNIG. :: :: EPEDKFENMG.	AKLVQDVANN : :: AQMVKEVASK	TNEEAGDGT::::	TTATVLARSI::::::	PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTTTATVLARSIAKEGFEKISKGANPVEI::::::::::::::::::::::::::::::::::::	GANPVEI:::GMNPMDL
	141	150	160	170	180	190	200	210
HUMP1 GROEL	RRGVM :: KRGIDI	LAVDAVIAE. ::: KAVTAAVEE	LKKQSKPVTT:::::::::::::::::::::::::::::::::::	PEEIAQVATI :::::: SKAIAQVGTI	SANGDKEIG:::::	NIISDAMKKV:::::	RRGVMLAVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDE :: :: :: :: :: :: :: :: :: :: :: :: ::	GKTLNDE : :: GTGLQDE
,	211	220	230	240	250	260	270	280
HUMP1 GROEL	LEIIEC	LEIIEGMKFDRGYIS; : :::::: LDVVEGMQFDRGYLSI	SPYFINTSKG( :::::: SPYFINKPETC	OKCEFQDAYV : SAVELESPFI	LLSEKKISS:::::LADKKISN	LEIIEGMKFDRGYISPYFINTSKGOKCEFQDAYVLLSEKKISSIQSIVPALEIANAHRKPLV : :::::::::::::::::::::::::::::::::::	PYFINTSKGOKCEFQDAYVLLSEKKISSIQSIVPALEIANAHRKPLVIIAEDVDG::::: ::::::::::::::::::::::::::::::	IIAEDVDG ::::::: IIAEDVEG
	281	290	300	310	320	330	340	350
HUMP1 GROEL	EALSTI ::: : EALATA	CVLNRLKVGI : :	GOVVAVKAPGF : :::::: /KVAAVKAPGF	GDNRKNQLKI :: :: GDRRKAMLQI	DMAIATGGA' : : : :: DIATLTGGT'	VFGEEGLTLNI : :: : VISEE-IGMEI	EALSTLVLNRLKVGLQVVAVKAPGFGDNRKNQLKDMAIATGGAVFGEEGLTLNLEDVQPHDLGKVGEVIV :::::::::::::::::::::::::::::::::::	CVGEVIV : DAKRVVI
	351	360	370	380	390	400	410	420
HUMP1	TKDDAM	ILLKGKGDKA	MIEKRIQEII	EQLDVTTSE	YEKEKLNERI	, LAKLSDGVAVI	ILLKGKGDKAQIEKRIQEIIEQLDVTTSEYEKEKLNERLAKLSDGVAVLKVGGTSDVEVNEKKDR	, NEKKDR
GROEL	NKDTTT	: : : !IIDGVGEEA	: AIQGRVAQIR	: :: QQIEEATSDY	: :: :: YDREKLQER\	::: ::: JAKLAGGVAVI	IDGVGEEAAIQGRVAQIRQQIEEATSDYDREKLQERVAKLAGGVAVIKVGAATEVEMKEKKAR	:::: IKEKKAR



Richard A. Young, et al. Inventors:

	421	430	440	450	460	470	480	490
HUMP1	VTDAL	NATRAAVE	EGIVLGGG	VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIIKRTLKIPAMTIAKNAGVEGSLI	TPANEDQKIG	IEIIKRTLF :	KIPAMTIAKNAGV	EGSLI
GROEL	VEDAL	HATRAAVE	EGVVAGGG	VEDALHATRAAVEEGVVAGGGVALIRVASKLADLRGQNEDQNVVSSSL-RAMEAPLRQIVLNCGEEPSVV	RGQNEDQNVV	7SSSL-RAME	3APLRQIVLNCGE	EPSVV
	491	200	510	520	530	540	550	560
HUMP1	VEKIM	QSSSEVGY	(DAMAGDFV	VEKIMQSSSEVGYDANAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMGA	VRTALLDAAG	SVASLLTTAF	EVVVTEIPKEEKD:	PGMGA ::
GROEL	ANTVK	GGDGNYGY	KNAATEEYG	ANTVKGGDGNYGYNAATEEYGNMIDMGILDPTKVTRSALQYAASVAGLMITTECMVTDLPKND-AADLGA	TRSALQYAAS	SVAGLMITTE	ECMVTDLPKND-A	ADLGA
	561	570						
HUMP1	MGGMG	MGGMGGGMGGGMF	3MF					
GROEL	AGGMG	AGGMGGMGGMM-	- MI					
Total 276	Total score = 276 identiti	4667, 5 breaks es out of 545	breaks of 545 po	4667, 5 breaks es out of 545 possible matches between residues	s between	residues		
25 random Alignment	random runs qnment score	11	65.34 SD	Standard deviation	iation =	18.94	Mean = $3429.48$	48



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Title: Stress Proteins and Uses Therefor

Richard A. Young, et al. Inventors:

HUMP1	1 , MLRLP9	10 ' TVFRQMRP	20 , VSRVLAPHLTF	30 ' IAYAKDVKFGA	40 , DARALMLQG	50 , VDĽĽAĎAVA	10 20 30 40 50 60 70 '''''''''''''''''''''''''''''''''''	TEQSWGS
ML65K				:: AKTIAYDE	: : EARRGLERG	LNSLADAVK	:: :: :: :: :: :: :: :: :: :: :: :: ::	LEKKWGA
	71	80	06	100	110	120	130	140
HUMP1 ML65K	PKVTKD::::		IDLKDKYKNIG: :::	AKLVQDVANN' : :: :: AELVKEVAKK'	TNEEAGDGT:::::	TTATVLARS:::::::	OGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTTTATVLARSIAKEGFEKISKGANPVEI :: :: :: :: :: :: :: :: :: :: :: :: ::	GANPVEI::
	141	150	160	170	180	190	. 200	210
HUMP1 ML65K	RRGVI :: KRGIE	ILAVDAVIA :::: :KAVDKVTE	ELKKQSKPVT1 : : : : TLLKDAKEVE1	PEEIAQVATI : :: : 'KEQIAATAAI	SANGDKEIG:::::SA-GDQSIG	NIISDAMKK:::::	RRGVMLAVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDE :: ::: ::: :: : : : : : : : : : : : :	GKTLNDE : SNTFGLQ
	211	220	230	240	250	260	270	280
HUMP1 ML65K	LEIIE ::: LELTE	LEIIEGMKFDRGYI :: :::::: LELTEGMRFDKGYI	ISPYFINTSKG :: :: ISGYFVTDAER	QKCEFQDAYV] : :QEAVLEEPYI]	LLSEKKISS:::::::::::::::::::::::::::::::::	IQSIVPALE : :: VKDLLPLLE	LEIIEGMKFDRGYISPYFINTSKGQKCEFQDAYVLLSEKKISSIQSIVPALEIANAHRKPLVIIAEDVDG :: ::::::::::::::::::::::::::::::::::	IAEDVDG::::::
	281	290	300	310	320	330	340	350
HUMP1 ML65K	EALSTL::::EALSTL	'LVLNRLKV' ::: 'LVVNKIRG'	GLQVVAVKAPG ::::::: TFKSVAVKAPG	FGDNRKNQLKI ::: :: : FGDRRKAMLQI	OMAIATGGA' ::::: OMAILTGAQ'	VFGEEGLTE:	VLNRLKVGLQVVAVKAPGFGDNRKNQLKDMAIATGGAVFGEEGLTLNLEDVQPHDLGKVGEVIV : : ::::::::::::::::::::::::::::::::	KVGEVIV : : KARKVVM
	351	360	370	380	390	400	410	420
ниме1	TKDDAM	MLLKGKGD	KAQIEKRIQEI : ::	IEQLDVTTSE:	YEKEKLNER.	LAKLSDGVA	LLKGKGDKAQIEKRIQEIIEQLDVTTSEYEKEKLNERLAKLSDGVAVLKVGGTSDVEVNEKKDR	VNEKKDR: : :
ML65K	TKDETT	TIVEGAGD	TDAIAGRVAQI	RTEIENSDSD	YDREKLQER	LAKLAGGVA	'IVEGAGDTDAIAGRVAQIRTEIENSDSDYDREKLQERLAKLAGGVAVIKAGAATEVELKERKHR	ткевкня



Inventors:

	421		430 4	440	450	460	470	480	490
HUMP1		VTDALNATI	RAAVEEGIVL	GGGCALLR	', NATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDOKIGIETIKRTLKIPAMTTAKNAGVEGSLT	PANEDOKIG	, TETTKRPL	, KTPAMTTAKN	A GVEGST. T
ML65K		:: [EDAVRNA]	::::::::::::::::::::::::::::::::::::::	::: GGGVTLLQ	::::::::::::::::::::::::::::::::::::::	TGDEAT-G	GANIVKVALEAPLK	EAPLKQIAFNS	SGMEPGVV
	491		500 5	510	520	530	540	550	560
HUMPI		VEKIMQSS	SEVGYDAMAG	DFVNMVEK	QSSSEVGYDAMAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMGA	, TALLDAAG	VASLLTTA	, EVVVTEIPKE	FKDPGMGA
ML65K		:: \EKVRNLS\	: : VGHGLNAATG	EYEDLLKA	AEKVRNLSVGHGLNAATGEYEDLLKAGVADPVKVTRSALQNAASIAGLFTT-EAVVADKPEKTAAPASDP	:: ::	: : :: IAGLFTT-	: :: : EAVVADKPEK	TAAPASDP
	561		570						
HUMP1		MGGMGGGMF	GGGMF						
ML65K		:::::: TGGMGG-MDF	JF						
Total 255		i ti	4552, 7 breaks es out of 540 p	s possibl	4552, 7 breaks es out of 540 possible matches between residues	between	residues		
25 random Alignment		runs score =	47.73 SD		Standard deviation =	tion =	23.86	Mean = 3413 16	3 16



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	٦,	10	20	30	40	50	09	70
HUMP1 TB65K	MLRLP:	TVFRQMRPV	SRVLAPHLTR	AYAKDVKFGA :: AKTIAYDE	DARALMLQGV :: EARRGLERGI	/DLLADAVAV ::::: .NALADAVKV	PTVFRQMRPVSRVLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTVIIEQSWGS :: ::::: :: :: :: :: :: :: :: :: :- :	SQSWGS :: :KKWGA
	71	80	06	100	110	120	130	140
нимр1 тв65к	PKVTK : : PTITN	DGVTVAKSI:::	DLKDKYKNIG : : : ELEDPYEKIG	AKLVQDVANN : :: :: AELVKEVAKK	TNEEAGDGTT::::::::::::::::::::::::::::::::::	TTATVLARSI <i>I</i> :::::: :TATVLAQALI	KDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTTTATVLARSIAKEGFEKISKGANPVEI::::::::::::::::::::::::::::::::::::	NPVEI ::
	141	150	160	170	180	190	200	210
HUMP1 TB65K	RRGVM :: KRGIE	LAVDAVIAE :: KAVEKVTET	LKKQSKPVTT : : : : LLKGAKEVET	PEEIAQVATI : :: : KEQIAATAAI	SANGDKEIGN:::::	VIISDAMKKVO : :::	MLAVDAVĪAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDE :: : : : : : : : : : : : : : : : : : :	TLNDE:
	211	220	230	240	250	260	270	280
HUMP1 TB65K	LEIIE ::: LELTE	GMKFDRGYI::::::GMRFDKGYI	SPYFINTSKG : :: SGYFVTDPER	QKCEFQDAYV : :: QEAVLEDPYI	LLSEKKISSI :: : LLVSSKVSTV	OSIVPALEIN : :: 7KDLLPLLEKN	EGMKFDRGYISPYFINTSKGQKCEFQDAYVLLSEKKISSIQSIVPALEIANAHRKPLVIIAEDVDG ::: :: :: :: :: :: : : : : : : : : : :	REDVDG
	281	290	300	310	320	330	340	350
нимг1 Тв65к	EALST:	LVLNRLKVG: :: : LVVNKIRGT!	LQVVAVKAPG :::::: FKSVAVKAPG	FGDNRKNQLK:::::::::	DMAIATGGAV :::::::: DMAILTGGQV	rgeegltini :: :: /ISEE-VGLTI	TLVLNRLKVGLQVVAVKAPGFGDNRKNQLKDMAIATGGAVFGEEGLTLNLEDVQPHDLGKVGEVIV :::::::::::::::::::::::::::::::::::	GEVIV :: RKVVV
	351	360	370	380	390	400	410	420
HUMP1 TB65K	TKDDA ::: TKDET	MLLKGKGDK: : :: TIVEGAGDTI	AQIEKRIQEI : : DAIAGRVAQI	IEQLDVTTSE : RQEIENSDSD	YEKEKLNERI : ::: ::: YDREKLQERI	AKLSDGVAVI	AMLLKGKGDKAQIEKRIQEIIEQLDVTTSEYEKEKLNERLAKLSDGVAVLKVGGTSDVEVNEKKDR : : : : : : : : : : : : : : : : : : :	IEKKDR : : : KERKHR



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Inventors:

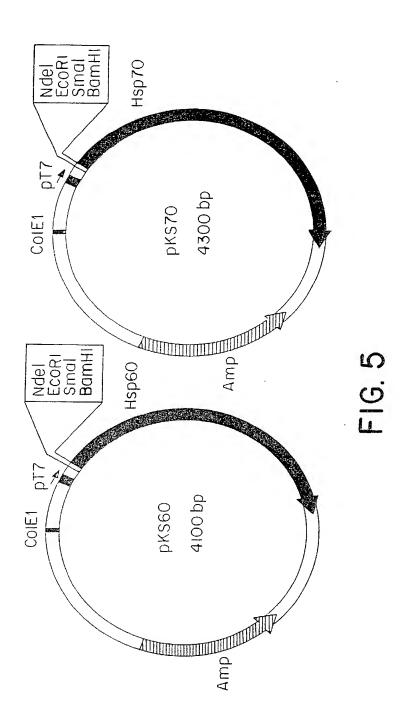
Richard A. Young, et al.

	421	430	440	450	460	470	480	490
HUMP1	VTDALN	ATRAAVEEG	; :IVLGGGCALLR(	CIPALDSLTP	ANEDQKIG	IEIIKRTLK	VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIIKRTLKIPAMTIAKNAGVEGSLI	EGSLI
TB65K	:: IEDAVR	::::: NAKAAVEEG	::::::::::::::::::::::::::::::::::::::	AAPTLDELK-	: : LEGDEATG.	ANIVKVALE	:: :::::::::::::::::::::::::::::::::::	: EPGVV
	491	500	510	520	530	540	550	560
HUMP1	VEKIMQ	SSSEVGYDA	AMAGDFVNHVEKO	SIIDPTKVVR	TALLDAAG	VASLLTTAE	VEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMGA	PGMGA
TB65K	AEKVRN	LPAGHGLNA	QTGVYEDLLAAC	SVADPVKVTR	SALQNAAS	IAGLFLTTE	AEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTRSALQNAASIAGLFLTTEAVVADKPEKEKASVPG-	SVPG-
	561	570						
HUMP1	MGGMGG	MGGMGGGMF						
TB65K	99	:::::: GGDMGGMDF						
Total 257	score = 4 identitie	4560, 5 breaks es out of 540	4560, 5 breaks es out of 540 possible matches between residue	e matches	between	residues		
25 ran Aliqnm	25 random runs Aliqnment score	t!	49.36 SD Stand	Standard deviation	tion =	23.23	23.23 Mean = 3413.16	16



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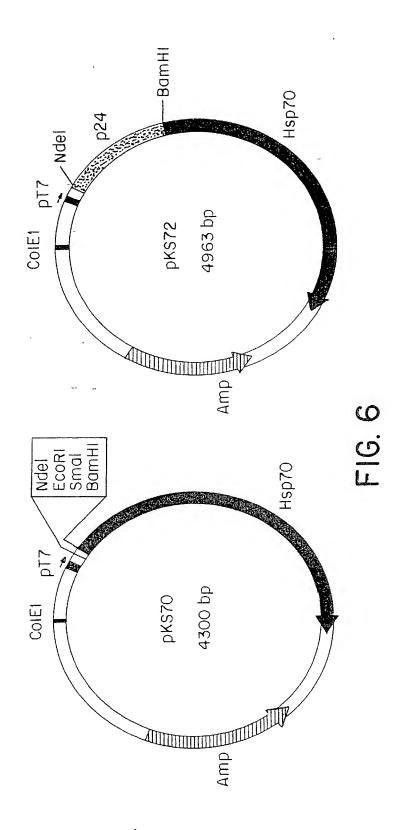
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